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Sequence Listing was accepted with existing errors.

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Reviewer: Keisha Douglas

Timestamp: Thu Jul 19 16:46:16 EDT 2007

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Application No: 10633484 Version No: 1.1

Input Set:

Output Set:

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Total Warnings: 0

Total Errors: 0

No. of SeqIDs Defined: 14

Actual SeqID Count: 14

SEQUENCE LISTING

<110> Rudiger Ridder, et.al.

<120> Method for solution based diagnosis

<130> 05033.0003.00US00

<140> 10/633,484

<141> 2003-07-31

<150> EP 02017313.4

<151> 2002-08-01

<160> 14

<170> PatentIn version 3.3

<210> 1

<211> 745

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(745)

<223> gamma-Catenin, Swissprot Accession Q86W21

<400> 1

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Gln	Gln	Thr	Tyr	Thr	Tyr	Asp	Ser	Gly	Ile	His	Ser	Gly	Ala	Asn	Thr
		20						25					30		

Cys	Val	Pro	Ser	Val	Ser	Ser	Lys	Gly	Ile	Met	Glu	Glu	Asp	Glu	Ala
	35						40					45			

Cys	Gly	Arg	Gln	Tyr	Thr	Leu	Lys	Lys	Thr	Thr	Thr	Tyr	Thr	Gln	Gly
	50					55					60				

Val	Pro	Pro	Ser	Gln	Gly	Asp	Leu	Glu	Tyr	Gln	Met	Ser	Thr	Thr	Ala
65				70						75					80

Arg	Ala	Lys	Arg	Val	Arg	Glu	Ala	Met	Cys	Ser	Gly	Val	Ser	Gly	Glu
			85						90					95	

Asp	Ser	Ser	Leu	Leu	Leu	Ala	Thr	Gln	Val	Glu	Gly	Gln	Ala	Thr	Asn
			100					105					110		

Leu Gln Arg Leu Ala Glu Pro Ser Gln Leu Leu Lys Ser Ala Ile Val
115 120 125

His Leu Ile Asn Tyr Gln Asp Asp Ala Glu Leu Ala Thr Arg Ala Leu
130 135 140

Pro Glu Leu Thr Lys Leu Leu Asn Asp Glu Asp Pro Val Val Val Thr
145 150 155 160

Lys Ala Ala Met Ile Val Asn Gln Leu Ser Lys Lys Glu Ala Ser Arg
165 170 175

Arg Ala Leu Met Gly Ser Pro Gln Leu Val Ala Ala Val Val Arg Thr
180 185 190

Met Gln Asn Thr Ser Asp Leu Asp Thr Ala Arg Cys Thr Thr Ser Ile
195 200 205

Leu His Asn Leu Ser His His Arg Glu Gly Leu Leu Ala Ile Phe Lys
210 215 220

Ser Gly Gly Ile Pro Ala Leu Val Arg Met Leu Ser Ser Pro Val Glu
225 230 235 240

Ser Val Leu Phe Tyr Ala Ile Thr Thr Leu His Asn Leu Leu Leu Tyr
245 250 255

Gln Glu Gly Ala Lys Met Ala Val Arg Leu Ala Asp Gly Leu Gln Lys
260 265 270

Met Val Pro Leu Leu Asn Lys Asn Asn Pro Lys Phe Leu Ala Ile Thr
275 280 285

Thr Asp Cys Leu Gln Leu Leu Ala Tyr Gly Asn Gln Glu Ser Lys Leu
290 295 300

Ile Ile Leu Ala Asn Gly Gly Pro Gln Ala Leu Val Gln Ile Met Arg
305 310 315 320

Asn Tyr Ser Tyr Glu Lys Leu Leu Trp Thr Thr Ser Arg Val Leu Lys
325 330 335

Val	Leu	Ser	Val	Cys	Pro	Ser	Asn	Lys	Pro	Ala	Ile	Val	Glu	Ala	Gly	340	345	350
Gly	Met	Gln	Ala	Leu	Gly	Lys	His	Leu	Thr	Ser	Asn	Ser	Pro	Arg	Leu	355	360	365
Val	Gln	Asn	Cys	Leu	Trp	Thr	Leu	Arg	Asn	Leu	Ser	Asp	Val	Ala	Thr	370	375	380
Lys	Gln	Glu	Gly	Leu	Glu	Ser	Val	Leu	Lys	Ile	Leu	Val	Asn	Gln	Leu	385	390	395
Ser	Val	Asp	Asp	Val	Asn	Val	Leu	Thr	Cys	Ala	Thr	Gly	Thr	Leu	Ser	405	410	415
Asn	Leu	Thr	Cys	Asn	Asn	Ser	Lys	Asn	Lys	Thr	Leu	Val	Thr	Gln	Asn	420	425	430
Ser	Gly	Val	Glu	Ala	Leu	Ile	His	Ala	Ile	Leu	Arg	Ala	Gly	Asp	Lys	435	440	445
Asp	Asp	Ile	Thr	Glu	Pro	Ala	Val	Cys	Ala	Leu	Arg	His	Leu	Thr	Ser	450	455	460
Arg	His	Pro	Glu	Ala	Glu	Met	Ala	Gln	Asn	Ser	Val	Arg	Leu	Asn	Tyr	465	470	475
Gly	Ile	Pro	Ala	Ile	Val	Lys	Leu	Leu	Asn	Gln	Pro	Asn	Gln	Trp	Pro	485	490	495
Leu	Val	Lys	Ala	Thr	Ile	Gly	Leu	Ile	Arg	Asn	Leu	Ala	Leu	Cys	Pro	500	505	510
Ala	Asn	His	Ala	Pro	Leu	Gln	Glu	Ala	Ala	Val	Ile	Pro	Arg	Leu	Val	515	520	525
Gln	Leu	Leu	Val	Lys	Ala	His	Gln	Asp	Ala	Gln	Arg	His	Val	Ala	Ala	530	535	540
Gly	Thr	Gln	Gln	Pro	Tyr	Thr	Asp	Gly	Val	Arg	Met	Glu	Glu	Ile	Val	545	550	555
																		560

Glu Gly Cys Thr Gly Ala Leu His Ile Leu Ala Arg Asp Pro Met Asn
565 570 575

Arg Met Glu Ile Phe Arg Leu Asn Thr Ile Pro Leu Phe Val Gln Leu
580 585 590

Leu Tyr Ser Ser Val Glu Asn Ile Gln Arg Val Ala Ala Gly Val Leu
595 600 605

Cys Glu Leu Ala Gln Asp Lys Glu Ala Ala Asp Ala Ile Asp Ala Glu
610 615 620

Gly Ala Ser Ala Pro Leu Met Glu Leu Leu His Ser Arg Asn Glu Gly
625 630 635 640

Thr Ala Thr Tyr Ala Ala Ala Val Leu Phe Arg Ile Ser Glu Asp Lys
645 650 655

Asn Pro Asp Tyr Arg Lys Arg Val Ser Val Glu Leu Thr Asn Ser Leu
660 665 670

Phe Lys His Asp Pro Ala Ala Trp Glu Ala Ala Gln Ser Met Ile Pro
675 680 685

Ile Asn Glu Pro Tyr Gly Asp Asp Leu Asp Ala Thr Tyr Arg Pro Met
690 695 700

Tyr Ser Ser Asp Val Pro Leu Asp Pro Leu Glu Met His Met Asp Met
705 710 715 720

Asp Gly Asp Tyr Pro Ile Asp Thr Tyr Ser Asp Gly Leu Arg Pro Pro
725 730 735

Tyr Pro Thr Ala Asp His Met Leu Ala
740 745

<210> 2
<211> 314
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(314)

<223> Ep-Cam, Swissprot Accession P16422

<400> 2

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1 5 10 15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
50 55 60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
100 105 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
165 170 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
180 185 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
195 200 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser

210

215

220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
 225 230 235 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
 245 250 255

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
 260 265 270

Val Val Val Val Met Ala Val Val Ala Gly Ile Val Val Leu Val Ile
 275 280 285

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
 290 295 300

Met Gly Glu Met His Arg Glu Leu Asn Ala
 305 310

<210> 3
 <211> 882
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(882)
 <223> E-Cadherin, Swissprot Accession P12830

<400> 3

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Val Ser Ser Trp Leu Cys Gln Glu Pro Glu Pro Cys His Pro Gly Phe
 20 25 30

Asp Ala Glu Ser Tyr Thr Phe Thr Val Pro Arg Arg His Leu Glu Arg
 35 40 45

Gly Arg Val Leu Gly Arg Val Asn Phe Glu Asp Cys Thr Gly Arg Gln
 50 55 60

Arg Thr Ala Tyr Phe Ser Leu Asp Thr Arg Phe Lys Val Gly Thr Asp

65		70		75		80
Gly Val Ile Thr Val Lys Arg Pro Leu Arg Phe His Asn Pro Gln Ile						
	85		90		95	
His Phe Leu Val Tyr Ala Trp Asp Ser Thr Tyr Arg Lys Phe Ser Thr						
	100		105		110	
Lys Val Thr Leu Asn Thr Val Gly His His His Arg Pro Pro Pro His						
	115		120		125	
Gln Ala Ser Val Ser Gly Ile Gln Ala Glu Leu Leu Thr Phe Pro Asn						
	130		135		140	
Ser Ser Pro Gly Leu Arg Arg Gln Lys Arg Asp Trp Val Ile Pro Pro						
145		150		155		160
Ile Ser Cys Pro Glu Asn Glu Lys Gly Pro Phe Pro Lys Asn Leu Val						
	165		170		175	
Gln Ile Lys Ser Asn Lys Asp Lys Glu Gly Lys Val Phe Tyr Ser Ile						
	180		185		190	
Thr Gly Gln Gly Ala Asp Thr Pro Pro Val Gly Val Phe Ile Ile Glu						
	195		200		205	
Arg Glu Thr Gly Trp Leu Lys Val Thr Glu Pro Leu Asp Arg Glu Arg						
	210		215		220	
Ile Ala Thr Tyr Thr Leu Phe Ser His Ala Val Ser Ser Asn Gly Asn						
225		230		235		240
Ala Val Glu Asp Pro Met Glu Ile Leu Ile Thr Val Thr Asp Gln Asn						
	245		250		255	
Asp Asn Lys Pro Glu Phe Thr Gln Glu Val Phe Lys Gly Ser Val Met						
	260		265		270	
Glu Gly Ala Leu Pro Gly Thr Ser Val Met Glu Val Thr Ala Thr Asp						
	275		280		285	
Ala Asp Asp Asp Val Asn Thr Tyr Asn Ala Ala Ile Ala Tyr Thr Ile						
	290		295		300	

Leu Ser Gln Asp Pro Glu Leu Pro Asp Lys Asn Met Phe Thr Ile Asn
305 310 315 320

Arg Asn Thr Gly Val Ile Ser Val Val Thr Thr Gly Leu Asp Arg Glu
325 330 335

Ser Phe Pro Thr Tyr Thr Leu Val Val Gln Ala Ala Asp Leu Gln Gly
340 345 350

Glu Gly Leu Ser Thr Thr Ala Thr Ala Val Ile Thr Val Thr Asp Thr
355 360 365

Asn Asp Asn Pro Pro Ile Phe Asn Pro Thr Thr Tyr Lys Gly Gln Val
370 375 380

Pro Glu Asn Glu Ala Asn Val Val Ile Thr Thr Leu Lys Val Thr Asp
385 390 395 400

Ala Asp Ala Pro Asn Thr Pro Ala Trp Glu Ala Val Tyr Thr Ile Leu
405 410 415

Asn Asp Asp Gly Gly Gln Phe Val Val Thr Thr Asn Pro Val Asn Asn
420 425 430

Asp Gly Ile Leu Lys Thr Ala Lys Gly Leu Asp Phe Glu Ala Lys Gln
435 440 445

Gln Tyr Ile Leu His Val Ala Val Thr Asn Val Val Pro Phe Glu Val
450 455 460

Ser Leu Thr Thr Ser Thr Ala Thr Val Thr Val Asp Val Leu Asp Val
465 470 475 480

Asn Glu Ala Pro Ile Phe Val Pro Pro Glu Lys Arg Val Glu Val Ser
485 490 495

Glu Asp Phe Gly Val Gly Gln Glu Ile Thr Ser Tyr Thr Ala Gln Glu
500 505 510

Pro Asp Thr Phe Met Glu Gln Lys Ile Thr Tyr Arg Ile Trp Arg Asp
515 520 525

Thr	Ala	Asn	Trp	Leu	Glu	Ile	Asn	Pro	Asp	Thr	Gly	Ala	Ile	Ser	Thr	530	535	540	
Arg	Ala	Glu	Leu	Asp	Arg	Glu	Asp	Phe	Glu	His	Val	Lys	Asn	Ser	Thr	545	550	555	560
Tyr	Thr	Ala	Leu	Ile	Ile	Ala	Thr	Asp	Asn	Gly	Ser	Pro	Val	Ala	Thr	565	570	575	
Gly	Thr	Gly	Thr	Leu	Leu	Leu	Ile	Leu	Ser	Asp	Val	Asn	Asp	Asn	Ala	580	585	590	
Pro	Ile	Pro	Glu	Pro	Arg	Thr	Ile	Phe	Phe	Cys	Glu	Arg	Asn	Pro	Lys	595	600	605	
Pro	Gln	Val	Ile	Asn	Ile	Ile	Asp	Ala	Asp	Leu	Pro	Pro	Asn	Thr	Ser	610	615	620	
Pro	Phe	Thr	Ala	Glu	Leu	Thr	His	Gly	Ala	Ser	Ala	Asn	Trp	Thr	Ile	625	630	635	640
Gln	Tyr	Asn	Asp	Pro	Thr	Gln	Glu	Ser	Ile	Ile	Leu	Lys	Pro	Lys	Met	645	650	655	
Ala	Leu	Glu	Val	Gly	Asp	Tyr	Lys	Ile	Asn	Leu	Lys	Leu	Met	Asp	Asn	660	665	670	
Gln	Asn	Lys	Asp	Gln	Val	Thr	Thr	Leu	Glu	Val	Ser	Val	Cys	Asp	Cys	675	680	685	
Glu	Gly	Ala	Ala	Gly	Val	Cys	Arg	Lys	Ala	Gln	Pro	Val	Glu	Ala	Gly	690	695	700	
Leu	Gln	Ile	Pro	Ala	Ile	Leu	Gly	Ile	Leu	Gly	Gly	Ile	Leu	Ala	Leu	705	710	715	720
Leu	Ile	Leu	Ile	Leu	Leu	Leu	Leu	Leu	Phe	Leu	Arg	Arg	Arg	Ala	Val	725	730	735	
Val	Lys	Glu	Pro	Leu	Leu	Pro	Pro	Glu	Asp	Asp	Thr	Arg	Asp	Asn	Val	740	745	750	

Tyr Tyr Tyr Asp Glu Glu Gly Gly Gly Glu Glu Asp Gln Asp Phe Asp
755 760 765

Leu Ser Gln Leu His Arg Gly Leu Asp Ala Arg Pro Glu Val Thr Arg
770 775 780

Asn Asp Val Ala Pro Thr Leu Met Ser Val Pro Arg Tyr Leu Pro Arg
785 790 795 800

Pro Ala Asn Pro Asp Glu Ile Gly Asn Phe Ile Asp Glu Asn Leu Lys
805 810 815

Ala Ala Asp Thr Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Leu Val
820 825 830

Phe Asp Tyr Glu Gly Ser Gly Ser Glu Ala Ala Ser Leu Ser Ser Leu
835 840 845

Asn Ser Ser Glu Ser Asp Lys Asp Gln Asp Tyr Asp Tyr Leu Asn Glu
850 855 860

Trp Gly Asn Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Glu
865 870 875 880

Asp Asp

<210> 4
<211> 906
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(906)
<223> Alpha-1 Catenin, Swissprot Accession P35221

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